AMENDMENTS TO THE CLAIMS

1. (Currently Amended) A method for calibrating data scanned from a molecular array, the method comprising:

selecting a molecular array that includes a set of calibrating features, each containing calibrating probes that hybridize to a majority ~~sufficient fraction~~ of target molecules in sample solutions to which the molecular array is intended to be exposed to produce corresponding signal intensities upon reading of the calibrating probes proportional to the total concentration of target molecules in the sample solutions, and a set of features containing probes that hybridize to specific target molecules under stringent conditions;

exposing the molecular array to a sample solution;

reading the molecular array to determine individual signal intensities for features and calibrating features of the molecular array;

calculating a collective calibration signal intensity from the signal intensities read from the ~~entire~~ set of calibrating features; and

calculating normalized signal intensities of the features containing probes that hybridize to specific target molecules, based on signal intensities read from features of the molecular array by applying to the signal intensities a normalization function that includes the calculated collective calibration signal.

2. (Original) The method of claim 1 wherein probes contained in the molecular array are oligonucleotides complementary to cDNA copies of cDNA transcripts of eukaryotic mRNA molecules and wherein the calibrating probes are poly(A) oligonucleotides.

3. (Original) The method of claim 1 wherein probes contained in the molecular array are oligonucleotides complementary to cRNA copies complementary to eukaryotic mRNA molecules and wherein the calibrating probes are poly(A) oligonucleotides.

4. (Original) The method of claim 1 wherein probes contained in the molecular array are oligonucleotides complementary to cDNA copies of cDNA transcripts of human mRNA molecules and

wherein the calibrating probes are oligonucleotides complementary to cDNA transcripts of Alu repeat sequences common to many human mRNAs.

5. (Original) The method of claim 1 wherein probes contained in the molecular array are oligonucleotides complementary to cDNA copies of the mRNA molecules and wherein the calibrating probes are oligonucleotides complementary to a synthetic nucleotide sequence appended to primers for reverse transcription of the mRNA molecules.

6. (Original) The method of claim 1 wherein probes contained in the molecular array are oligonucleotides complementary to cDNA copies of the mRNA molecules and wherein the calibrating probes are random-sequence oligonucleotides.

7. (Original) The method of claim 1

wherein calculating a collective calibration signal intensity from the signal intensities read from the set of calibrating features further includes calculating a set of collective calibration signal intensities by partitioning the signal intensities generated from the set of calibrating features into sets of similar calibrating signal intensities and calculating a collective signal intensity for each set, so that the sets of similar calibrating signal intensities each covers a discrete range of signal intensities and so that the discrete ranges of signal intensities span an overall range of signal intensities generated from features of the molecular array, and

wherein calculating normalized signal intensities based on signal intensities read from features of the molecular array by applying to the signal intensities a normalization function that includes the calculated collective calibration signal further includes applying to each signal intensity a normalization function that includes the calculated collective calibration signal calculated from the set of calibrating signal intensities within the discrete range of intensities in which the signal intensity generated from the feature of the molecular array is included.

8. (Original) The method of claim 1

wherein calculating a collective calibration signal intensity from the signal intensities read from the set of calibrating features further includes calculating the average calibration signal intensity from the signal intensities read from the set of calibrating features, and

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wherein calculating normalized signal intensities based on signal intensities read from features of the molecular array by applying to the signal intensities a normalization function that includes the calculated collective calibration signal further includes dividing each signal intensity by the calculated average calibration signal intensity.

9. (Canceled)

10. (Currently Amended) A method for calibrating data scanned from a molecular array, the method comprising:

selecting a molecular array that includes features and that includes a calibration feature that includes calibrating probes that hybridize to a majority of target molecules in sample solutions, the calibration feature thereby producing a signal intensity directly proportional to the total concentration of target molecules in the sample solutions;

exposing the molecular array to a sample solution;

reading the molecular array to determine signal intensities for the features of the molecular array and for the calibrating feature; and

calculating normalized signal intensities for the features, each normalized signal intensity based on the determined signal intensity for the respective feature and the signal intensity generated by the calibration probe, and each normalized signal intensity being directly mathematically ~~functionally~~ related to a mole fraction of sample molecules that hybridize to the respective feature and inversely mathematically related to a mole fraction of sample molecules that hybridize to the calibration feature.

11. (Currently Amended) The method of claim 10 wherein a plurality ~~number~~ of calibration features are included in the molecular array, each calibration feature including calibrating probes that hybridize to a majority of target molecules in sample solutions, each said ~~the~~ calibration feature thereby producing a signal intensity directly proportional to the total concentration of target molecules in the sample solutions.

12. (Currently Amended) The method of claim 11 wherein a collective calibration signal intensity is calculated from signal intensities read from said plurality ~~the number~~ of calibration features, and wherein calculating normalized signal intensities for the features further comprises calculating normalized signal intensities based on the signal intensities read from the features of the molecular array

by applying to the signal intensities a normalization function that includes the calculated collective calibration signal.

13. (Canceled)

14. (Canceled)

15. (New) The method of claim 1, wherein an average of the signal intensities read from the calibrating features is proportional to the total concentration of target molecules in the sample solution to which the array is exposed.

16. (Withdrawn) A method for calibrating data scanned from a molecular array, the method comprising:

selecting a molecular array that includes a set of calibrating features containing calibrating probes that hybridize to a sufficient fraction of target molecules of a sample to which the molecular array is intended to be exposed to produce corresponding signal intensities upon reading of the calibrating probes proportional to the total concentration of target molecules in the sample solution, and a set of features containing probes that hybridize to specific target molecules in the sample solution under stringent conditions;

exposing the molecular array to a sample solution;

determining a mole fraction of sample molecules that hybridize to the calibration features; and

calculating normalized signal intensity of a feature containing probes that hybridize to a specific target molecule, based on a mole fraction of the sample molecules that hybridize to the feature containing probes that hybridize to a specific target molecule and the mole fraction of sample molecules that hybridize to the calibration features.